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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/903,925

DATE: 12/07/2001
TIME: 17:47:27

Input Set : N:\Crf3\RULE60\09903925.txt
Output Set: N:\CRF3\12072001\I903925.raw

3 <110> APPLICANT: Genentech, Inc.
4 Ashkenazi, Avi
5 Botstein, David
6 Desnoyers, Luc
7 Eaton, Dan L.
8 Ferrara, Napoleone
9 Filvaroff, Ellen
10 Fong, Sherman
11 Gao, Wei-Qiang
12 Gerber, Hanspeter
13 Gerritsen, Mary E.
14 Goddard, A.
15 Godowski, Paul J.
16 Grimaldi, Christopher J.
17 Gurney, Austin L.
18 Hillan, Kenneth, J.
19 Kljavin, Ivar J.
20 Mather, Jennie P.
21 Pan, James
22 Paoni, Nicholas F.
23 Roy, Margaret Ann
24 Stewart, Timothy A.
25 Tumas, Daniel
26 Williams, P. Mickey
27 Wood, William, I.
29 <120> TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
30 Acids Encoding the Same
32 <130> FILE REFERENCE: 10466-14
34 <140> CURRENT APPLICATION NUMBER: 09/903,925
35 <141> CURRENT FILING DATE: 2001-07-11
37 <150> PRIOR APPLICATION NUMBER: 09/665,350
38 <151> PRIOR FILING DATE: 2000-09-18
40 <150> PRIOR APPLICATION NUMBER: PCT/US00/04414
41 <151> PRIOR FILING DATE: 2000-02-22
43 <150> PRIOR APPLICATION NUMBER: US 60/143,048
44 <151> PRIOR FILING DATE: 1999-07-07
46 <150> PRIOR APPLICATION NUMBER: US 60/145,698
47 <151> PRIOR FILING DATE: 1999-07-26
49 <150> PRIOR APPLICATION NUMBER: US 60/146,222
50 <151> PRIOR FILING DATE: 1999-07-28
52 <150> PRIOR APPLICATION NUMBER: PCT/US99/20594
53 <151> PRIOR FILING DATE: 1999-09-08
55 <150> PRIOR APPLICATION NUMBER: PCT/US99/20944
56 <151> PRIOR FILING DATE: 1999-09-13
58 <150> PRIOR APPLICATION NUMBER: PCT/US99/21090
59 <151> PRIOR FILING DATE: 1999-09-15
61 <150> PRIOR APPLICATION NUMBER: PCT/US99/21547

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65 <151> PRIOR FILING DATE: 1999-10-05
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68 <151> PRIOR FILING DATE: 1999-11-29
70 <150> PRIOR APPLICATION NUMBER: PCT/US99/28313
71 <151> PRIOR FILING DATE: 1999-11-30
73 <150> PRIOR APPLICATION NUMBER: PCT/US99/28564
74 <151> PRIOR FILING DATE: 1999-12-02
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77 <151> PRIOR FILING DATE: 1999-12-02
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83 <151> PRIOR FILING DATE: 1999-12-20
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104 tggagctccg gctgcgtctt cccgcagcgc taccgcccat gcgcctgccg 150
106 cgccggggccg cgctggggct cctgccgctt ctgctgctgc tgccgcccgc 200
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118 tggctgcagc tgaagagcga atatcctgac ttattcgagt ggttttgtgt 500
120 gaagacactg aaagtgtgct gctctccagg aacctacggt cccgactgtc 550
122 tcgcatgcca gggcggatcc cagaggccct gcagcgggaa tggccactgc 600
124 agcggagatg ggagcagaca gggcgacggg tcctgccggt gccacatggg 650
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132 ggtgctggac gaggggcgct gtgtggatgt ggacgagtgt gcggccgagc 850
134 cgctccctg cagcgtgctg cagttctgta agaacgccaa cggctcctac 900
136 acgtgcgaag agtgtgactc cagctgtgtg ggctgcacag gggaaggccc 950
138 aggaaactgt aaagagtgtg tctctggcta cgcgaggagg cacggacagt 1000
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150 gtggccctga ggatgccgtc tcctgcagtg gacagcggcg gggagaggct 1300
154 gcctgctctc taacggttga ttctcatttg tcccttaaac agctgcattt 1350
156 cttggttggt cttaaacaga cttgtatatt ttgatacagt tctttgtaat 1400
158 aaaattgacc attgtaggta atcaggagga aaaaaaaaaa aaaaaaaaaa 1450
160 aaagggcggc cgcgactcta gagtcgacct gcagaagctt ggccgccatg 1500
162 gcccaacttg tttattgcag cttataatgg ttacaaataa agcaatagca 1550
164 tcacaaattt cacaaataaa gcattttttt cactgcattc tagttgtggt 1600
166 ttgtccaaac tcatcaatgt atcttatcat gtctggatcg ggaattaatt 1650
168 cggcgcagca ccatggcctg aaataacctc tgaaagagga acttggttag 1700
170 gtaccttctg aggcggaaag aaccagctgt ggaatgtgtg tcagttaggg 1750
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174 ctcaattagt cagcaaccca gtttt 1825

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176 <210> SEQ ID NO: 2

177 <211> LENGTH: 353

178 <212> TYPE: PRT

179 <213> ORGANISM: Homo Sapien

181 <400> SEQUENCE: 2

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185 Leu Leu Leu Pro Pro Ala Pro Glu Ala Ala Lys Lys Pro Thr Pro
186 20 25 30
188 Cys His Arg Cys Arg Gly Leu Val Asp Lys Phe Asn Gln Gly Met
189 35 40 45
191 Val Asp Thr Ala Lys Lys Asn Phe Gly Gly Gly Asn Thr Ala Trp
192 50 55 60
194 Glu Glu Lys Thr Leu Ser Lys Tyr Glu Ser Ser Glu Ile Arg Leu
195 65 70 75
197 Leu Glu Ile Leu Glu Gly Leu Cys Glu Ser Ser Asp Phe Glu Cys
198 80 85 90
200 Asn Gln Met Leu Glu Ala Gln Glu Glu His Leu Glu Ala Trp Trp
201 95 100 105
203 Leu Gln Leu Lys Ser Glu Tyr Pro Asp Leu Phe Glu Trp Phe Cys
204 110 115 120
206 Val Lys Thr Leu Lys Val Cys Cys Ser Pro Gly Thr Tyr Gly Pro
207 125 130 135
209 Asp Cys Leu Ala Cys Gln Gly Gly Ser Gln Arg Pro Cys Ser Gly
210 140 145 150
212 Asn Gly His Cys Ser Gly Asp Gly Ser Arg Gln Gly Asp Gly Ser
213 155 160 165
215 Cys Arg Cys His Met Gly Tyr Gln Gly Pro Leu Cys Thr Asp Cys
216 170 175 180
219 Met Asp Gly Tyr Phe Ser Ser Leu Arg Asn Glu Thr His Ser Ile
220 185 190 195
222 Cys Thr Ala Cys Asp Glu Ser Cys Lys Thr Cys Ser Gly Leu Thr
223 200 205 210
225 Asn Arg Asp Cys Gly Glu Cys Glu Val Gly Trp Val Leu Asp Glu
226 215 220 225
228 Gly Ala Cys Val Asp Val Asp Glu Cys Ala Ala Glu Pro Pro Pro

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232		245		250		255
234	Cys Glu Glu Cys	Asp Ser Ser Cys Val	Gly Cys Thr Gly Glu	Gly		
235		260		265		270
237	Pro Gly Asn Cys	Lys Glu Cys Ile Ser	Gly Tyr Ala Arg Glu	His		
238		275		280		285
240	Gly Gln Cys Ala	Asp Val Asp Glu Cys	Ser Leu Ala Glu Lys	Thr		
241		290		295		300
243	Cys Val Arg Lys	Asn Glu Asn Cys Tyr	Asn Thr Pro Gly Ser	Tyr		
244		305		310		315
246	Val Cys Val Cys	Pro Asp Gly Phe Glu	Glu Thr Glu Asp Ala	Cys		
247		320		325		330
249	Val Pro Pro Ala	Glu Ala Glu Ala Thr	Glu Gly Glu Ser Pro	Thr		
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265	cgcccagccg	tctaaacggg	aacagccctg	gctgagggag	ctgcagcgca	150
267	gcagagtatc	tgacggcgcc	aggttgcgta	ggtgcggcac	gaggagtttt	200
269	cccggcagcg	aggaggtcct	gagcagcatg	gcccggagga	gcgccttccc	250
271	tgccgcgcg	ctctggtct	ggagcatcct	cctgtgcctg	ctggcactgc	300
273	ggggcgaggc	cgggcccgcg	caggaggaga	gcctgtacct	atggatcgat	350
275	gctcaccagg	caagagtact	cataggattt	gaagaagata	tcctgattgt	400
277	ttcagagggg	aaaatggcac	cttttacaca	tgatttcaga	aaagcgcaac	450
279	agagaatgcc	agctattcct	gtcaatatcc	attccatgaa	ttttacctgg	500
281	caagctgcag	ggcaggcaga	atacttctat	gaattcctgt	ccttgcgctc	550
284	cctggataaa	ggcatcatgg	cagatccaac	cgtcfaatgtc	cctctgctgg	600
286	gaacagtgcc	tcacaaggca	tcagttgttc	aagttggttt	cccatgtctt	650
288	ggaaaacagg	atgggggtgg	agcatttgaa	gtggatgtga	ttgttatgaa	700
290	ttctgaaggc	aacaccattc	tccaaacacc	tcaaaatgct	atcttcttta	750
292	aaacatgtca	acaagctgag	tgcccaggcg	ggtgccgaaa	tggaggcttt	800
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296	ctgtgagaaa	gccctttgta	ccccacgatg	tatgaatgg	ggactttgtg	900
298	tgactcctgg	tttctgcac	tgcccacctg	gattctatgg	agtgaactgt	950
300	gacaaagcaa	actgctcaac	cacctgcttt	aatggaggga	cctgtttcta	1000
302	ccctggaaaa	tgtatttgcc	ctccaggact	agaggagag	cagtgtgaaa	1050
304	tcagcaaagt	cccacaacc	tgctgaaatg	gaggtaaatg	cattggtaaa	1100
306	agcaaagtga	agtgttccaa	aggttaccag	ggagacctct	gttcaaagcc	1150
308	tgtctgcgag	cctggctgtg	gtgcacatgg	aacctgccat	gaaccaaca	1200
310	aatgccaatg	tcaagaaggt	tggcatggaa	gacactgcaa	taaaaggtag	1250
312	gaagccagcc	tcatacatgc	cctgaggcca	gcaggcgccc	agctcaggca	1300
314	gcacacgcct	tcacttaaaa	aggccgagga	gcggcgggat	ccacctgaat	1350

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316 ccaattacat ctggtgaact cgcacatctg aaacgtttta agttacacca 1400
318 agttcatagc ctttggttaac ctttcatgtg ttgaatgttc aaataatgtt 1450
320 cattacactt aagaatactg gcctgaattt tattagcttc attataaatc 1500
322 actgagctga tatttactct tccttttaag ttttctaagt acgtctgtag 1550
324 catgatggta tagattttct tgtttcagtg ctttgggaca gattttatat 1600
326 tatgtcaatt gatcagggtta aaattttcag tgtgtagttg gcagatattt 1650
328 tcaaaattac aatgcattta tgggtgtctgg gggcagggga acatcagaaa 1700
330 ggttaaattg ggcaaaaatg cgtaagtcac aagaatttgg atgggtgcagt 1750
332 taatgttgaa gttacagcat ttcagatttt attgtcagat atttagatgt 1800
334 ttgttacatt tttaaaaaatt gctcttaatt tttaaactct caatacaata 1850
336 tattttgacc ttaccattat tccagagatt cagtattaaa aaaaaaaaaa 1900
338 ttacactgtg gtagtggcat ttaaacaata taatatattc taaacacaat 1950
340 gaaataggga atataatgta tgaacttttt gcattggctt gaagcaatat 2000
342 aatatattgt aaacaaaaca cagctcttac ctaataaaca ttttatactg 2050
344 tttgtatgta taaaataaag gtgctgcttt agtttttttg aaaaaaaaaa 2100
346 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa gggcgggcgc gactctagag 2150
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353 <210> SEQ ID NO: 4

354 <211> LENGTH: 379

355 <212> TYPE: PRT

356 <213> ORGANISM: Homo Sapien

358 <400> SEQUENCE: 4

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363      20              25              30
365 Pro Gln Glu Glu Ser Leu Tyr Leu Trp Ile Asp Ala His Gln Ala
366      35              40              45
368 Arg Val Leu Ile Gly Phe Glu Glu Asp Ile Leu Ile Val Ser Glu
369      50              55              60
371 Gly Lys Met Ala Pro Phe Thr His Asp Phe Arg Lys Ala Gln Gln
372      65              70              75
374 Arg Met Pro Ala Ile Pro Val Asn Ile His Ser Met Asn Phe Thr
375      80              85              90
377 Trp Gln Ala Ala Gly Gln Ala Glu Tyr Phe Tyr Glu Phe Leu Ser
378      95              100             105
380 Leu Arg Ser Leu Asp Lys Gly Ile Met Ala Asp Pro Thr Val Asn
381      110             115             120
383 Val Pro Leu Leu Gly Thr Val Pro His Lys Ala Ser Val Val Gln
384      125             130             135
386 Val Gly Phe Pro Cys Leu Gly Lys Gln Asp Gly Val Ala Ala Phe
387      140             145             150
389 Glu Val Asp Val Ile Val Met Asn Ser Glu Gly Asn Thr Ile Leu
390      155             160             165
392 Gln Thr Pro Gln Asn Ala Ile Phe Phe Lys Thr Cys Gln Gln Ala
393      170             175             180
395 Glu Cys Pro Gly Gly Cys Arg Asn Gly Gly Phe Cys Asn Glu Arg
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VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\09903925.txt

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L:2197 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:50
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